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D14305 Hepatitis C
D17763 Hepatitis C
A40615 Sequence 15
A40621 Sequence 21
A40625 Sequence 25
A40627 Sequence 27
BD172131 New seque
BD172134 New seque
BD172136 New seque
BD172136 New seque
                 BD172132 New seque
AX031591 Sequence
AX031861 Sequence
AX031865 Sequence
AX032131 Sequence
AX032131 Sequence
AX032135 Sequence
L12355 Hepatitis C
A40619 Sequence
AX03137 Sequence
AX031597 Sequence
AX031867 Sequence
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Sequence 17
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1 (bases 1 to 447)

1 (bases 1 to 447)

Meartens,G. and Stuyver,L.

Meartens,G. and Stuyver,L.

NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC AGENTS

PATENT: WO 9613590-A 51 09-MAY-1996;

INNOENDALICS NV (BE)

Other publication Au 3844095 960523.
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                                                                                                                                                                                                                                                                                                                                            DNA

    447
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Sequence 51 from Patent WO9613590.
A50396
A50396.1 GI:2303407
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AX031595
AX031861
AX032136
AX03233
AX03233
HPCCOREH
HPCSTRUCTC
A40619
BA10513
AX031597
AX031597
AX031597
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A40621
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A40627
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BD172134
BD172136
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unidentified
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D49749 Hopatitis C
D49752 Hopatitis C
D49752 Hopatitis C
D49774 Hopatitis C
D49774 Hopatitis C
D49764 Hopatitis C
D16614 Hopatitis C
D16616 Hopatitis C
                                                                 4, 2005, 09:25:48; Search time 6803 Seconds (without alignments) 3183.813 Million cell updates/sec
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                                                                                                                                 1 gacggaattaatttcgcaac.....aggactgcaactgttccatc 447
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        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                  4708233 segs, 24227607955 residues
                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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HPCHCV048
HPCNE137B
HPCNE145G
HPCNE048A
HPCHCV049
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HPCJK07030A3

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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CTCTACATGGTAACTAACGACTGCAGTAACGGTAGTATCGTGTATGAGGCCGGGGATATT

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A40613 Sequence

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HPCCOREEAL 110-00T 447 bp 88-RNA linear VRL 16-OCT-2001 Hepatitis C virus type 3 clone NL96 precursor protein gene, partial
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van Doorn, L., Kleter, G.E., Stuyver, L., Maertens, G., Brouwer, J.T.,
Schalm, S.W., Heijtink, R.A. and Quint, W.G.
Sequence analysis of hepatitis C virus genotypes 1 to 5 reveals
multiple novel subtypes in the Benelux countries
J. Gen. Virol. 76 (Pt 7), 1871-1876 (1995)
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/db_xref="di:845494"
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                                                                                                                                                                                                                                                                                                                                          DNA stage; Flaviviridae;
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van Doorn, L.J., Kleter, B., Stuyver, L., Maertens, G., Brouwer, H.,
Schalm, S., Heijtink, R. and Quint, W.
Analysis of heparitis C virus genotypes by a line probe assay and
Correlation with antibody profiles
J. Hepatol. 21 (1), 122-129 (1994)
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Hepacivirus.
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/mol_type="genomic RNA"
/db xref="texon:40363"
/clone="NL96"
/note="genotype: 3"
           421 ACTGTCCAGGACTGCAACTGTTCCATC 447

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    /note="putative"

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/product="el protein"
/note="putative"
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Henatitis C virus type 3
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    ATCCTCCACTTACCTGGCTGTGTCCCCTGCGTACGCTCTGGCAATACATCAAGATGCTGG
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                                               ATCCTGTGAGCCCYACCGTCGCCGTGAAGTCGCCCTGCGCCCGCCACCGCCTCTCCGC
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Maertens, G. and Stuyver, L.
Maertens, G. and Stuyver, L.
Squences of hepatitis C virus genotypes and their use as prophylactic, therapeutic and diagnostic agents
Patent: US 6180768-A 51 30-UAN-2001;
Location/Qualifiers
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llarity 100.0%; Pred. No. 9.6e-109;
Conservative 0; Mismatches 0;
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Sequence 51 from patent US 6180768.
AR127536 1 GI:14114131
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Location/Qualifiers
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                                                            Length 1584;
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87.9%; Score 393; DB 14;
Best Local Similarity 91.9%; Pred. No. 1.5e-94;
Matches 411; Conservative 3; Mismatches 33;
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Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                  ACGCACCTGGATATGATGGTGGGRGCGGCCACCCTATGCTCAGCTCTCTACGTAGGAGAC 360
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181 ATCCTCCACTTACCTGGCTGTGTCCCCTGCGTACGCTCTGGCAATACATCAAGATGCTGG 240
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Submitted (17-MAR-1995) Hiroaki Okamoto, Jichi Medical School,
Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi
329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
Tel:0285-44-2111(ex.3334), Fax:0285-44-1557)
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GINFATGNLPGCSPSIFLLALLSCLLTPTAGLEYRNVSGLYIVTNDCSNSSIVYEAGD
IIIHHEGGVPCVRSGNTSRCWTPVSPFVANSRRBGATTASLRTHYDDWWGAATLCSALY
VGDLCGALFLVGGGFSWRRRQHWTVQECNCSIYPGHLTGHRWAWDMMMWSPAVTMVV
SQVLRLPGPTFDLVAGAHWGYMAGVAYYSMQGNWAKVFLVLCEFSGVDASTTISGGSA
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               Tokita, H., Okamoto, H., Iizuka, H., Kishimoto, J., Tsuda, F., Lesmana, L.A., Miyakawa, Y. and Mayumi, M. Hepatitis C virus variants from Jakarta, Indonesia classifiable into novel genotypes in the second (2e and 2f), tenth (10a) and eleventh (11a) genetic groups
J. Gen. Virol. 77 (Pt. 2), 293-301 (1996)
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Pred. No. 1.5e-94;
3; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                      organism="Hepatitis C virus"
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340. . . . 1584
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Best Local Similarity 91.9%;
Matches 411; Conservative 3
                                                                                                                                                                                                            Unpublished
3 (bases 1 to 1584)
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VGDLGGALFLVGQGFSWRHRQHWTVQDCNCSIYPGHLTGHRWAWDWWNGNAGTYVTNVV
SQVLRLPQTILDLVIGAHWWYMAGYYYSMQGNWAKVFLVLCFSGVDATTRITAGSA
AHSTRGFASLFTTGARQNLQLVN"
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3; Mismatches 33; Indels 0
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D49752.
D49752.1 GI:1197162
core, env, and part of E2/NS1.
Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no
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C virus"
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Hepatitis C virus isolate JK070 gene
                                                                                                               'evidence=not_experimental
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                                                                           Query Match 87.9%;
Best Local Similarity 91.9%;
Matches 411; Conservative
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HPCJK049El 9450 bp RNA linear VRL 13-FEB-1999 Hepatitis C virus isolate.JK049 genomic RNA for polyprotein,
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Hepatitis C virus
Hepatitis C virus
Viruses; seRNA positive-strand viruses, no DNA stage; Flaviviridae;
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SQVLRLPQTWPDLVIGAHWGVMAGVAYSMQGNWAKVPLVLCLFSGVDASTTITGGVA
ASGAFTITSLFSTGAKQPLHLVNTNGSWHINRTALNCNDSLNTGFIAGLLYYHKFNSS
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SRPSWGPNDPRRRSRNLGKVI DTLTCGFADLMGYI PLVGAPVGGVARALAHGVRALED
GINPATGNLPGCSFSI FLLALLSCLLTPTAGLEYRNASGLYTVTNDCSNGSI VYEAGD
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CFPSPWYVGAATDKRGAPTYTWGENBSDVFLLEBSARPPTBFWFGCTWWMGSGYVKTCG
APPCHIYGGREGKSNNSLVCFTDCFRKHPDATYNRCGAGPWLTPRCLVDYPYRLWHYP
CTVNYTIFKVRWFVGGLEHRPNAACNWTRGBRCNLEDBRRSEMYPLLHSTTEGABLLDF
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J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
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Submitted (10-AUG-1995) Hiroaki Okamoto, Jichi Medical School,
Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi
329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
Tel:0285-44-2111(ex.3334), Fax:0285-44-1557)
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D63821.1 GI:1183032
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2 (bases 1 to 9450)
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Unpublished
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             GCTTTGTTCTCATGCTTACACCCACAGCCGGGCTGGAGTACCGTAATGCCTCCGGA
                                                                                                                                                CTCTACATGGTAACTAACGACTGCAGTAACGGTAGTATCGTGTATGAGGCCGGGGATATT
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J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
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Submitted (17-MR-1995) Hiroaki Okamoto, Jichi Medical School,
Submitted (17-MR-1995) Hiroaki Okamoto, Jichi Medical School,
Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi
329-04, Japan (E-mail:Nokamoto@jichi.ac.jp,
Inolation/Qualifiers
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Hepatitis C virus is E2/NS1, partial cds.
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                                                         HPCJK030A3 1584 bp RNA linear VRL 10-FEB-1999 Hepatitis C virus isolate JK030 gene for core, env, and part of E2/NS1, partial cds.
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D49747.1 GI:1197102
Core, env. and part of E2/NS1.
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                     CTITGIGGAGCGCTATITCTTGTYGGGCAGGGGTTCTCATGGAGACATCGCCAGGAITGG 420
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Tokita, H., Okamoto, H., Iizuka, H., Kishimoto, J., Tsuda, F.,
Lesmana, L.A., Miyakawa, Y. and Mayumi, M.
Hepatitis C. virus variants from Jakarta, Indonesia classifiable
into novel genotypes in the second (2e and 2f), tenth (10a) and
eleventh (11a) genetic groups
J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
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Direct Submission
Submitted (17-MAR-1995) Hiroaki Okamoto, Jichi Medical School,
Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi
329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
Tel:0285-44-2111(ex.3334), Fax:0285-44-1557)
Location/Qualifiers
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87.2%; Score 389.8; DB 14; Length 1584;
Best Local Similarity 91.5%; Pred. No. 1.1e-93;
Matches 409; Conservative 3; Mismatches 35; Indels 0;
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larity 91.3%; Pred. No. 3e-93;
Conservative 3; Mismatches 36; Indels 0;
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citation=[2]
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Hepatitis C virus (individual isolate Td-3/93) gene for polyprotein precursor, partial cds (core protein (carboxy terminus) and El B10046 D30046.1 GI:485798
El envelope protein; core protein.
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hotta, H., Handajani, R., Lusida, M.I., Soemarto, W., Doi, H., Miyajima, H. and Homma, M. Subrype analysis of hepatitis C virus in Indonesia on the basis NS5b region sequences
J. Clin. Microbiol. 32 (12), 3049-3051 (1994) (BiteB) LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

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/translation="LSCLLTPTAGLEYRNASGLYIVTNDCSNSSIVYEAODIILHMPG
CDPCVRSGNTSRCWTPVSSTVAVGRAGAATASLRTHVDMMVGAATLCSALYVGDLCGA
LFLVGQGFSWRHRQHWTVQDCNCSIYPGHLTGHRM"
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                                                                            Direct Submission
Submitted (28-APR-1994) Hak Hotta, Kobe University School of
Medicine, Department of Microbiology; 7-5-1 Kusunoki-cho, Chuo-ku,
Kobe, Hyogo 650, Japan (Tel:078-341-7451(ex.3301),
Pax:078-331-6347)
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Pred. No. 9.9e-76;
3; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="polyprotein precursor"
protein id="BAA06282.1"
db xref="G1:485799"
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Hepatitis C virus"
/mol type="genomic RNA"
/isoTate="rd-3/93"
                                                                                                                                                                                Submitted (28-Apr-1994) to DDBJ by:
Hak Hotta
                                                                                                                                                                                                                        Kobe University School of Medicine
Department of Microbiology
7-5-1 Kusunoki-cho, Chuo-ku
Kobe, Hyogo 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:11103"
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Best Local Similarity 90.0%;
Matches 342; Conservative 3
           Hotta, H.
Unpublished
3 (bases 1 to 411)
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                                   858 CTATACATACTTACCAACGACTGCTCTAACAGCAGCATCGTGTATGAGGCTGATAATGTC 917
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Hepatitis C virus RNA for core, env,and part of E2/NSI polyprotein.
D16620
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Hepatitis C virus
Hepatitis C virus
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                                                                                                         181 ATCCTCCACTTACCTGGCTGTGCCTTGCGTACGCTCTGGCAATACATCAAGATGCTGG
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Tokite, H., Shrestha,S.M., Okamoto,H., Sakamoto,M., Horikita,M.,
Iizuka,H., Shrestha,S., Miyakawa,Y. and Mayumi,M.
Hepatitis C virus variants from Nepal with novel genotypes and
their classification into the third major group
J. Gen. Virol. 75 (Pt 4), 931-936 (1994)
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/evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Hepatitis C 'mol type="genomic RNA" /isolate="NE274"
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GVRAVRKSSERSQPRGRRQPIPKARRSEGRSWAQPGYPWPLYGNEGCGWAGWILSPRG
SRPSWGPNDPRRRSRNLGKVIDTLTCGFADLMGYIFLVGAPVGGVARALAHGVRALED
GINFATGNLPGCSFSIFLLALFSCLVSPAAGLEYRNTSGLYILTNDCSNSSIVYEADN
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VGDLCGAVFLVGQAFTFRARQHYTVQLCNCSLYPGHITGHHMANDMMMNSPTAALVV
AHLIRIPQTVFDMIVGAHWGVMAGLAYFAMQGNWAKVGIVLILFSGVDADTCTTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                        Shrestha, S.M., Tsuda, F., Okamoto, H., Tokita, H., Horikita, M., Tanaka, T., Miyakawa, Y. and Mayumi, M. Hepatitis B virus subtypes and hepatitis C virus genotypes in patients with chronic liver disease in Nepal Hepatology 19 (4), 805-809 (1994)
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Hiroaki Okamoto
Immunology Division
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/translation="MSTLPKPQRKTKRNTIRRPQDVKFPGGGQIVGGVYLLPRRGPRL
VRVAVRKTSERSEPRNRRQPIPKARESEGRS#AQPGYPWPLYGNBGGGWAGFLLSPRG
SRPSWGPNDPRRSRUGKVIDTLTCRSFALDMGVIPLVGAPVGGVARALAHGVYBALED
GINFATGNLPGGSFSIFLLALDSCLVCPADAGIEYRNVSGLYVLTNDGSNGSIVYEAPE
VILHLPGGVPPCVQSGNSSQCWIPVAPVKYAGATTASIRSHVDLLVGAATLCSALY
AHVLALPCTIFDIIAGNAFTRRPRQBNTVQTCNCSLYPGHLSGHRMAMDMMNWSPRVGLVV
AHVLALPCTIFDIIAGNAFTRAGIAAGLAYYSMQTNWAKVPIIIVMFSGVDARTHTTGGVA
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Direct Submission

Direct Submission

Submitted (08-7UL-1993) Tomoyoshi Ohno, Nagoya City University

Medical School, Second Department of Internal Medicine; 1-1

Kawasumi, Mizuho, Nagoya, Aichi 467, Japan

(Tel:052-851-5511(ex.8748,2265), Fax:052-852-0849)

Location/Qualifiers

1. .867

/organism="Hepatitis C virus"

/mol_type="genomic RNA"
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Tokite, H., Shreetha, S.M., Okamoto, H., Sakamoto, M., Horikita, M., Tizuka, H., Shreetha, S., Miyakawa, Y. and Mayumi, M. Hizuka, H., Shreetha, S., Miyakawa, Y. and Mayumi, M. Hepatitis C virus variants from Nepal with novel genotypes and their classification into the third major group

Gen. Virol. 75 (Pt 4), 931-936 (1994)
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Janeshar, S.M., Tsuda, F., Okamoto, H., Tokita, H., Horikita, M., Tanaka, T., Miyakawa, Y. and Mayumi, M.

Tanaka, T., Miyakawa, Y. and Mayumi, M.

Hepatitis B virus subtypes and hepatitis C virus genotypes patients with chronic liver disease in Nepal

Hepatology 19 (4), 805-809 (1994)
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                                                                          Score 244.4; DB 14; Length
Pred. No. 1.1e-54;
); Mismatches 126; Indels
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D16616.1 GI:475870
E2/NS1; core protein; envelope protein.
Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no
                                                                                                                                                       GACGGAATTAATTTCGCAACAGGGAATTTACCTGGTTGC
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env, and
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Submitted (06-JUL-1993) to
Hiroaki Okamoto
                                                                        Query Match
Best Local Similarity 71.7%; Pre
Matches 320; Conservative 0;
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Jichi Medical School
Kawachi-gun
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                                                                                                 1 (bases 1 to 447).

Van Doorn, L.J., Kleter, B., Stuyver, L., Maertens, G., Brouwer, H., Schalm, S., Heijtink, R. and Quint, W.

Analysis of hepatitis C virus genotypes by a line probe assay and correlation with antibody profiles
J. Hepatol. 21 (1), 122-129 (1994)
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                                                                                                                                                                                                                                                                                                  van Doorn, L.J., Klter, G.E., Stuyver, L., Maertens, G., Schalm, S.W., Heijtink, R.A. and Quint, W.G. Sequence analysis of hepatitis C virus genotypes 1 to multiple novel subtypes in the Benelux countries J. Gen. Virol. 76 (Pt 7), 1871-1876 (1995)
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                Hepatitis C virus type 3a Hepatitis C virus type 3a Viruses; ssRNA positive-strand viruses; Hepacivirus.
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                                                                                                                                                                                                                                                                                                         /evidence=not experimental
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SHAMRLPGFFFDL.AGAHWGVMAGLAYFSMQGNWARVGIVLIMFSGVDAETHVTGGTV
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                                                                                                             1. .1504
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0285-44-1557.
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421 ACTGTCCAGGACTGCAACTGTTC 443 || || || || || || || || || || || 421 ACGGTCCAGACTTGTAACTGCTC 443

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'cgnz 6/ptodata1/ina/6A_COMB.seq:*
'cgnz 6/ptodata1/ina/6B_COMB.seq:*
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US-09-878-281A-15
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US-09-878-281A-25
US-09-878-281A-25
US-09-878-281A-23
US-09-878-281A-13
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Listing first 45 summaries
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28 199.4 44.6 742 1 US-08-081-072-18 Sequence 18, Appl 199.4 44.6 742 1 US-08-449-093A-18 Sequence 18, Appl 31 199.4 44.6 932 1 US-08-449-093A-15 Sequence 15, Appl 32 1 US-08-449-093A-15 Sequence 15, Appl 32 1 US-08-816-075A-35 Sequence 15, Appl 34 196.2 44.3 447 3 US-08-816-075A-35 Sequence 35, Appl 34 196.2 43.9 501 2 US-08-481-055-30 Sequence 31, Appl 36 196.2 43.9 501 2 US-08-481-231 Sequence 30, Appl 36 196.2 43.9 501 2 US-08-487-231-30 Sequence 30, Appl 36 196.2 43.9 501 2 US-08-487-231-30 Sequence 30, Appl 36 196.2 43.9 501 2 US-08-612-973-7 Sequence 30, Appl 37 196.2 43.9 501 3 US-08-612-973-7 Sequence 7, Appl 41 196.2 43.9 795 3 US-08-612-973-7 Sequence 5, Appl 41 196.2 43.9 795 3 US-08-612-973-4 Sequence 5, Appl 41 196.2 43.9 2082 3 US-08-612-973-4 Sequence 6, Appl 41 196.2 43.9 2082 3 US-08-612-973-4 Sequence 6, Appl 41 196.2 43.9 2082 3 US-08-612-973-4 Sequence 47, Appl 41 196.2 43.9 2082 3 US-08-612-973-4 Sequence 49, Appl 42 196.2 43.9 2082 3 US-08-612-973-4 Sequence 49, Appl 42 196.2 43.9 2082 3 US-08-612-973-4 Sequence 49, Appl 44 196.2 43.9 2082 3 US-08-612-973-4 Sequence 49, Appl 45 196.2 43.9 2082 3 US-08-612-973-4 Sequence 49, Appl 45 196.2 43.9 2082 3 US-08-612-973-4 Sequence 49, Appl 45 196.2 43.9 2082 3 US-08-612-973-4 Sequence 49, Appl 45 196.2 43.9 2082 3 US-08-612-973-4 Sequence 49, Appl 45 196.2 43.9 2082 3 US-08-612-973-4 Sequence 49, Appl 45 196.2 43.9 2082 3 US-08-612-973-4 Sequence 49, Appl
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ALIGNMENTS

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RESULT 1
US-08-836-075A-51
US-08-836-075A-51
Sequence 51, Application US/08836075A
Patent No. 6180768
Patent No. 6180768
Fatent No. 6180768
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
TITLE OF INVENTION: AGENTS
TITLE OF INVENTION: AGENTS
TITLE OF INVENTION: AGENTS
CORRESPONDENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSER: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
TEXAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

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ZIP: 77210-43

ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Location disk
COMPUTER: Laboration disk
COMPUTE
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us-09-851-138c-51.rni

December 447; December 447; December 447; December 447; December 447; December 447; December 60; December 60;	300 US-09-878-281A-17 Sequence 17, Application US/091 Sequence 17, Application US/091 360 APPLICANT: Innogenetics N.V. TITLE OF INVENTION: New sequence 17 TITLE OF INVENTION: NEW T	Guery Match genotypes for diagnosis, propt Db 62 Qy 61 Db 122 Qy 121 Db 122	Length 541; Length 541; Db 242 ATTCTCCACTTACCTGGCTGTGTCTCCCTGCGCATACATCAGGTGTGTGT
Local Similarity 100.0%; Pred. No. 19-124; Lemgin 447; Conservative 0; Mismatches 0; Indels 0; Gaps 1 dacGGAATTAATTTCGCAACAGGGAATTTACCTGGTTGCTCTTTCTT		Sequence 13, Application US/09878281A Patent No. 6762024 GENERAL INFORMATION: APPLICANT: Innogenetics N.V. TITLE OF INVENTION: New sequences of hepatitis C virus TITLE OF INVENTION: and therapy FILE REFERENCE: 35 CURRENT APPLICATION NUMBER: US/09/878,281A CURRENT FILING DATE: 2001-06-12 NUMBER OF SEQ ID NOS: 284 SOFTWARE: Patentin version 3.1 SEQ ID NO 13 LENGTH: 541 TYPE: DNA CURRENTSM: hepatitis C virus US-09-878-281A-13	Query Match 52.8%; Score 236.2; DB 4; Length 541; Best Local Similarity 70.7%; Pred. No. 2.9e-61; Matches 313; Conservative 1; Mismatches 129; Indels 0; Gaps GacGGGATAATTTCGCAACAGGGAATTTACCTGGTTGCTCTTTCTT

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RESULT 6
US-09-878-281A-21
Sequence 21, Application US/09878281A
Patent No. 6762024
GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: and therapy
TITLE OF INVENTION: and therapy
FILE REFERENCE: 35
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOFTWARE: Patentin version 3.1
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                                                                                                            Score 233; DB 4; Length 541;
Pred. No. 2.7e-60;
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                                                                                                                                                      1; Mismatches 131; Indels
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Pred. No. 2.7e-60;
1; Mismatches 131; Indels
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                                                                                                            52.1%;
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Best Local Similarity 70.2%;
Matches 311; Conservative
                      TYPE: DNA ORGANISM: hepatitis C virus
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                                                                                                                                Best Local Similarity 70.2
Matches 311; Conservative
                                                       7 OKGANIZANI 115 US-09-878-281A-15
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                                                                                                            Query Match
      LENGTH:
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                                                                                                                                                               APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph
TITLE OF INVENTION: and therapy
FILE REFERENCE: 35
CURRENT APPLICATION NUMBER: US/09/878,281A
CURRENT PILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOFTWARE: PATENTIN VETSION 3.1
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APPLICANT: Innogenetics N.V.
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis,
TITLE OF INVENTION: and therapy
FILE REFERENCE: 35
CURRENT APPLICATION NUMBER: US/09/878,281A
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOPTWARE: Patentin version 3.1
SEQ ID NO 15
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Pred. No. 8.9e-61;
1; Mismatches 130;
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  ACGGTCCAGACCTGTAACTGCTC 504
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                                                                                                     Sequence 19, Application US/09878281A
Patent No. 6762024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 70.4%;
Matches 312; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: hepatitis C virus US-09-878-281A-19
                                                                                                                                               GENERAL INFORMATION:
                                                                                 .09-878-281A-19
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US-09-878-281A-15
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LENGTH: 541
482
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	ORGANISM: hepatitis C virus	Qy 181 ATCTCCACTTACCTGGCTGTCCCTGCGTACGCATACATCAAGATGCTGG 240 Db 242 ATTCTGCACGCCGCGCTGTGTGTCCTGGCCCTCGCCCCCCTCTCTCCGC 301 Qy 241 ATCCCTGTGAGCCCTACCGTGAAGTCGCCTGCGCCGCCACCGCCTCTCTCCGC 300 Db 302 ACCCTGTGAGCCCTACGTGAGTCGCTGGCCTTCGATACGC 361 Qy 301 ACCACGTGAAATGATGGCGGCGCGCGCCCTTGGGCTTCGATACGC 361 Db 362 AGTCATGGGGGCGGCGCGCCCTTTACGTGGGCTTTACGTGGGTGAT 421 Qy 361 [RESULT 9 US-08-612-973-29 i Sequence 29, Application US/08612973 j Patent No. 6150134 j GENERAL INPRMATTON: APPLICANT: MAERTENS, GERT j APPLICANT: BOSMAN, FONS j APPLICANT: BUSMAN, FONS j APPLICANT: BUSKE, MARIE-ANGE
Qy 121 CTCTACATGGTAACTAACGACTGCAGTAACGGTAGTATCGTGTATGAGGCGGGGATATT 180 Bb 182 CTCTATGTCCTACCAACGACTGTTCCAATAGCAGTATTGTGTACGAGGCGGATGGTT 241 Qy 181 ATCCTCCACTTACCTGGCTGTGTCCCCTGCGTACGCTCTGGCAATACATCAGAGGTGGTG 240 Bb 242 ATTCTGCACATACCTGGCTGAACGTCAGGAGGAATACATCCACTGGGGAATACATCCACTGGGGAATACATCCACTGGGGAATACATCCACTGGGAATACATCCACTGGAATACATCGGGAATACATCCACTGGGAATACATCGGGAATACATCGGGAATACATCGGGAATACATCGGGAATACATCGGGAATACATCGGGAATACATCGGAATACATCGGAATACATCGGAATACATCGGAATACGTCGGAATACGGGAATACGTCGGAATACGTCAATACGTCGAATACGTCAATACGTCAATACGTCGAATACGTCAATACTCAATACGTCAATACGTCAATACGTCAATACGTCAATACGTCAATACGTCAATACGTCAATACGTCAATACGTCAATACGTCAATACGTCAATACTACAATA	RESULT 7 US-09-878-281A-25 i Sequence 25, Application US/09878281A i Patent No. 6762024 i GENERAL INFORMATION: i APPLICANT: Innogenetics N.V. i TITLE OF INVENTION: New Sequences of hepatitis C virus genotypes for diagnosis, proplication FILE REFERENCE: 35 i CURRENT APPLICATION NUMBER: US/09/878,281A i CURRENT APPLICATION NUMBER: US/09/878,281A i CURRENT FILING DATE: 2001-06-12 i NUMBER OF SEQ ID NOS: 284 i SEQ ID NO 25 i LENGTH: 541 i SEQ ID NO 25 i LENGTH: 541 i TYPE: DNA i TYPE: DNA i TYPE: DNA i CORANISM: hepatitis C virus US-09-878-281A-25	Query Match 52.1%; Score 233; DB 4; Length 541; Best Local Similarity 70.2%; Pred. No. 2.7e-60; Anatches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0; QY 1 GACGGGATTAATTCGCAACAGGGAATTTACCTGGTTGCTCTTTTCTTTC	Oy 241 ATCCTGTGAGCCCYACGGTGGAGTCGCCTGGGCCGCCGCCTCTCCGC 300 Db 302 ACCCCAGTAACACCTACAGTGGCAGTCAGGTACGTCGGGCACCACGCTTCGATACGC 361 Oy 301 ACGCACGTGGATATGATGGTGGGRGCGGCCACCCTATGCTCAGGTAGGAGAC 360 Db 362 AGTCATGTGGACTGTTAGTAGGCGCCACGATGTGCTCTGCGCTTTAGGTGGGTG

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61 GCTTTGTTCTCATGCTTGCTTACACCCACAGCCGGGCTGGAGTACCGTAATGCCTCCGGA 120
                                      484 ATGTGTGGGGCTGTCTTCCTCGTGGGACAAGCCTTCACGTTCAGACCTCGTCGCCATCAA 543
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Patent No. 6245503

GENERAL INFORMATION:

APPLICANT: MAERTENS, GERT
APPLICANT: DE MARTYNOPF, GUY
APPLICANT: DE WARTYNOPF, GUY
APPLICANT: DE WARTYNOPF, GUY
APPLICANT: DE NUSEL-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDRAB:
APPLICATION UNDRAB:
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                         544 ACGGTCCAGACCTGTAACTGCTC 566
                                                                                                        421 ACTGTCCAGGACTGCAACTGTTC 443
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TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 630 base pairs
TYPE: nucleic acid
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Matches 311; Conservative
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; LOCATION: 1..624
US-08-927-597-29
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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
STREET: 11
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FEATURE:
                                                                                                                                                                                                                                                                     RESULT 10
US-08-927-597-29
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                               PURIFIED HEPATITIS C VIRUS ENVELOPE
PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC
CORRESPONDENCE ADDRESS:

ADDRESSER: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ALLINGTON
STATE: VIRGHT AND ALLINGTON
STATE: VIRGHT AND ALLINGTON
STATE: VIRGHT AND ALLINGTON
STATE: VIRGHT AND ALLINGTON
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
COMPUTER: IJ-WAR-1996
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
FILING DATE: 11-WAR-1996
CLASSIPICATION WUMBER: 32,205
REFERRICE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
THORMATION FOR SEC ID NO:
SECURE TELECOMMUNICATION INFORMATION:
THORMATION FOR SEC ID NO:
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Pred. No. 2.9e-60;
1; Mismatches 131; Indels
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Best Local Similarity 70.2
Matches 311; Conservative
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LOCATION:
FEATURE:
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US-08-612-973-29
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Qy 121 CTCTACATGGTAACTAACGACTGCAGTAACGGTAGTATCGTGTATGAGGCCGGGGGATATT 180 Db 244 CTCTATGTCTTACCTGTTCCAATAGCAGTATTGTGTAGGAGGCCGATGACGTT 303 Qy 181 ATCCTCCACTTACCTGGGTGCTCCTGCGTAGGATACAATACAATACATGAGGGGG 240 Db 304 ATTCTGCACCACCCGCTGCATACCTTGTGTCCAGGACGCAATACATCCACGTGCTGG 363	QY 361 CTTTGTGGAGCGCTATTTCTTGTYGGCGAGGGTTCTCATGGACATCGCCAGCATTGG 420 bb 422 ATGTGTGGGCCGTCTTCCTCGTGGGACAAGCCTTCAGACCCCGCCGCCGCCATCAA 481 QY 421 ACTGTCCAGGACTGCTTC 443 bb 482 ACGTCCAGACTGCTTC 504
QY 241 ATCCCTGTGAGCCCYACGTGGCGTGAAGTGGCCCTGGGCGCCCACCGCCTCTCTCGGC 300 Db 364 ACCCCAGTGACACCTACAGTCAAGTACGTCGGAGCAACCACCTTCGATACGC 423 QY 301 ACGCACGTGGATATGATGGTGGGGCGCCCCTATGCTCAGCTCTCTACGTAGAGAC 360 Db 424 AGTCATGTGGACCTATTAGTGGGCGCGCCCCCATGCTCTCCGCTCTACCTGGGTTAC 1	RESULT 12 US-09-878-281A-177 ; Sequence 177, Application US/09878281A ; Patent No. 6762024 ; ARENEAL INFORMATION: ; APPLICANT: Innogenetics N.V. ; TITHE OF INVENTION:
	(878,281A
Qy 421 ACTGTCCAGGACTGCTC 443	Ø
81.8	ORGANISM: -09-878-2817 Query Match Best Local E
illle OF INVENTION: New Sequences of hepatitis C virus genotypes for diagnosis, proph; TITLE OF INVENTION: and therapy; TITLE OF INVENTION: and therapy; TITLE OF INVENTION OF CURRENT APPLICATION NUMBER: US/09/878,281A; CURRENT FILING DATE: 2001-06-12; NUMBER OF SEQ ID NOS: 284; NUMBER OF SEQ ID NOS: 284; STATE OF SEQ ID NOS: 284	Qy 1 GACGGAATTACTCGCAACAGGAATTTACCTGGTTGCTCTTTCTCTATCTTCTG 60
; SEQ ID NO 23 ; LENGTH: 541 ; TYPE: DNA ; ORGANISM: hepatitis C virus US-09-878-281A-23	121
Query Match 51.8%; Score 231.4; DB 4; Length 541; Best Local Similarity 70.0%; Pred. No. 8.2e-60; Matches 310; Conservative 1; Mismatches 132; Indels 0; Gaps 0;	OY 181 ATCTCCACTTACCTGGCTGTGTCCCCTGCGTACGCTCTGGCAATACATCAAGATGCTGG 240
1 GACGGAATTAAATTTCGCAACAGGGAATTTACCTGGTTGCTCTTCTCTATCTTCC 	Oy 241 ATCCTGTGAGGCCYACGGTGAAGTCGCCCTGGGCGCCACCGCCTCTCTCCGC 300 140 ATTCCTTTAACACCCACTGTAGCCGTCCCTACCTCGGGGCTCCACTTACGTCTGTACGG 399
Qy 61 GCTTTGTTCTCATGCTTACACCCACAGCGGGCTGGAGTACCGTAATGCCTCCGGA 120 Db 122 GCTCTGTTCTTTATACATCCACAGCTGGTCTAAGAGTGGCGGAATACGTCTGC 181	Qy 301 ACGCACGTGGATATGATGGTGGGCGCCACCCTATGCTCAGCTCTCTACGTAGGAGAC 360
QY 121 CTCTACATGGTAACTGCAGTAACGGTAGTATCGTGTATGAGGCCGGGGATATT 180 DD 182 CTCTATGTCCTTACCAACGACTGTTCCAATAGTAGTATTGTGTATGAGGCCGATGACGTT 241	361 CITTGIGGAGGGTAITTCITGIYGGG
QY 181 AICCICCACITACCIGGCIGIGICCCCIGCGIACGCICTGGCAAIACAICAAGAIGCIGG 240	Oy 421 ACTGICCAGACTGITCCAIC 447
OY 241 AICCCTGIGAGCCCYACGICGCCGIGAAGTCGCCCTGCGCCACCGCCTCTCCCGC 300	RESULT 13 US-09-878-281A-120 ; Sequence 120, Application US/09878281A ; Patent No. 6/62024 ; CANERAL TURDWARTON.

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of hepatitis C virus genotypes for diagnosis, propi
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Pred. No. 4.2e-55;
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CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOFTWARE: Patentin version 3.1
SEQ ID NO 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 520 ACTACCCAGGACTGCAACTGCTCTATC 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 181, Application US/09878281A
; Patent No. 6762024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: New sequences
TITLE OF INVENTION: and therapy
FILE REFERENCE: 35
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Best Local Similarity 67.5%;
Matches 301; Conservative 1
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US-09-878-281A-181
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Patent NO. 6762024
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph
TITLE OF INVENTION: and therapy
FILE REPERBNCE: 35
CURRENT APPLICATION NUMBER: US/09/878,281A
CURRENT FILE OF INOS: 284
NUMBER OF SEC ID NOS: 284
SOFTWARE: PATENTIN version 3.1
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Pred. No. 4.2e-55;
2; Mismatches 144;
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Pred. No. 4.2e-55;
2; Mismatches 144;
FILE REFERENCE: 35
CURRENT APPLICATION NUMBER: US/09/878,281A
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOFTWARE: Patentin version 3.1
SEQ ID NO 120
LENGTH: 574
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Best Local Similarity 67.3%;
Matches 301; Conservative
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) ORGANISM: hepatitis C virus
US-09-878-281A-175
                                                                                                                                                 ORGANISM: hepatitis C virus US-09-878-281A-120
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US-09-878-281A-175
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LENGTH: 579
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cgn2 6/ptodata1//pna/US1012_COMB.seq:
cgn2 6/ptodata1//pna/US1013_COMB.seq:
cgn2 6/ptodata1//pna/US1013_COMB.seq:
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cgn2 6/ptodata1//pna/US107A_COMB.seq:
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cgn2 6/ptodata1//pna/US109_COMB.seq:
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cgn2 6/ptodata1//pna/US6002_COMB.seq:
cgn2 6/ptodata1//pna/US6003_COMB.seq:
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/cgn2_6/1
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'Cgn2_6' (ptodata)1/pna/PCTUS2_COMB.seq:*
'Cgn2_6' (ptodata)1/pna/US06_COMB.seq:*
'Cgn2_6' (ptodata)1/pna/US06_COMB.seq:*
'Cgn2_6' (ptodata)1/pna/US08_COMB.seq:*
'Cgn2_6' (ptodata)1/pna/US09_COMB.seq:*
'Cgn2_6' (ptodata)1/pna/US09_A' COMB.seq:*
'Cgn2_6' (ptodata)1/pna/US09_A' COMB.seq:*
'Cgn2_6' (ptodata)1/pna/US09_B' COMB.seq:*
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1/pna/US096C_COMB. seq: *
1/pna/US096C_COMB. seq: *
1/pna/US096C_COMB. seq: *
1/pna/US097B_COMB. seq: *
1/pna/US097B_COMB. seq: *
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1/pna/US098A_COMB. seq: *
1/pna/US098B_COMB. seq: *
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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'cgn2_6/ptodata/1/pna/US099E
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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COMB. Beq:

COMB. Beq:

pna/US6028_COMB.seg:*

COMB. seq:

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01.2-8 / 60

/ cgn2_6/ptodata/1/pna/US099F_COMB.seq:*
cgn2_6/ptodata/1/pna/US099G_COMB.seq:*
cgn2_6/ptodata/1/pna/US100A_COMB.seq:*
cgn2_6/ptodata/1/pna/US101A_COMB.seq:*
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cgn2_6/ptodata/1/pna/US107B_COMB.seq:*

RESULT 1
US-08-836-075A-51
; Sequence 51, Application US/08836075A
; GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
STUYVER
STUYVER

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| cgn2_6/ptodata/1/pna/US6048_COMB.seq:*
| cgn2_6/ptodata/1/pna/US6048_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 51, Appl Sequence 220, Appl Sequence 220, Appl Sequence 218, Appl Sequence 218, Appl Sequence 219, Appl Sequence 219, Appl Sequence 219, Appl Sequence 217, Appl Sequence 217, Appl Sequence 217, Appl Sequence 13, Appl Sequence 11, Appl Se Sequence 13, Sequence 17, Sequence 19, 1 Description 4 US-08-836-075A-51 4 US-08-836-075A-51 1 US-09-374-494-51 1 US-09-374-494-51 5 US-09-851-138-51 5 US-09-851-138-51 5 US-09-851-138-220 6 US-09-851-138-220 6 US-09-851-138-220 6 US-09-851-138-218 6 US-09-851-138-218 6 US-09-851-138-219 6 US-09-851-138-219 6 US-09-851-138-219 6 US-09-851-138-219 6 US-09-851-138-219 6 US-09-851-138-219 7 US-09-374-494A-217 6 US-09-374-494A-217 6 US-09-374-494A-217 7 US-09-851-138-217 8 US-08-36-455-13 8 US-08-36-455-13 8 US-09-873-224-13 7 US-09-873-224-13 7 US-09-873-224-13 8 US-09-89-046-17 8 US-09-89-046-19 8 US-09-89-046-19 8 US-09-89-046-19 8 US-09-89-046-19 SUMMARIES 4447 4447 9957 9957 9957 9957 9957 9957 Length Query Match 445.8 445.8 445.8 445.8 445.8 445.8 255.8 2555.8 2555.8 2555.8 2555.8 2555.8 2555.8 2555.8 2555.8 2555.8 236.6 236.6 236.6 236.6 236.6 236.2 236.2 236.2 236.2 238.2 Result Š.

STUTYER, LIEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC ó 120 120 180 180 240 240 300 301 ACGCACGTGGATATGATGGTGGGRGCGGCCACCCTATGCTCAGCTCTCTACGTAGGAGAC 360 9 9 GCTTTGTTCTCATGCTTGCTTACACCCACAGCCGGGCTGGAGTACCGTAATGCCTCCGGA ATCCTCCACTTACCTGGCTGTCCCCTGCGTACGCTCTGGCAATACATCAAGATGCTGG 181 ATCTCCACTTACCTGGCTGTGTCCCCTGCGTACGCTCTGGCAATAAGATGATGAGGTGG CTCTACATGGTAACTAACGACTGCAGTAACGGTAGTATCGTGTATGAGGCCGGGGATATT CTCTACATGGTAACTAACGACTGCAGTAACGGTAGTATCGTGTATATGAGGCCGGGGGATATT 241 ATCCTGTGAGCCCYACCGTCGCCGTGAAGTCGCCCTGCGCCGCCACCGCCTCTCTCCGC Gaps ; CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
COMPUTER: TEASA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,075A
FILING DATE: 21-Apr-1997
PRILING DATE: 23 Oct 1995
APPLICATION NUMBER: EP 94870166.9
FILING DATE: 21 Oct 1994
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 22 Jun 1995
APPLICATION NUMBER: EP 95870076.7 DB 14; Length 447; Indels 99.7%; Score 445.8; DB 14; 100.0%; Pred. No. 1.5e-114; cive 0; Mismatches 0; 1 GACGGAATTAATTTCGCAACAGGGAATTTACCTGGTTGCT NUMBER OF SEQUENCES: 207 CORRESPONDENCE ADDRESS: ADDRESSEE: ARNOLD, WHITE & DURKEE STREET: P.O. BOX 4443 NAME: KAMMERER, PATRICIA A. REGISTRATION NUMBER: 29,775 REFERENCE/DOCKET NUMBER: INNS:004 ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 51: INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA AGENTS ATTORNEY/AGENT INFORMATION Best Local Similarity 100. Matches 447; Conservative HYPOTHETICAL: NO US-08-836-075A-51 61 61 121 121 181 Query Match 8 셤 ò g qq ò 8 a à g ò

Sequence 19, Sequence 19, Sequence 19,

Sequence Sequence Sequence Sequence Sequence

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Sequence 51, Application US/09374494

GENERAL INFORMATION:
APPLICANT: MAERTENS, GERT
APPLICANT: STUVER, LIEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS
TITLE OF INVENTION: GENOTYPES AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND
TITLE OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD WHITE & DURKEE
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100.0%; Pred. No. 1.5e-114;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                         COMPUTER, 78 ADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compactible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GACGGAATTAATTTCGCAACAGGGAATTTACCTGGTTGC
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NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFRENCE/DOCKET NUMBER: INNU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713.787.1400
TELEFAX: 713.787.1440
                                                                                                                                                                                                 750 BERING DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.º
Matches 447; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                   CITY: HOUSTON
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                             ACGCACGTGGATATGATGGTGGGRGCGGCCACCCTATGCTCAGCTCTCTACGTAGGAGAC 360
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                                                                                                                                                                                                                                                                   Sequence 51, Application US/08836075B
GENERAL INFORMATION:
APPLICANT INNOGENETICS N.V.
ITLE OF INVENTION: Drophylactic, therapeutic and diagnostic agents.
TITLE OF INVENTION: Drophylactic, therapeutic and diagnostic agents.
FILE REPERENCE: 2551-105
CURRENT APPLICATION NUMBER: US/08/836,075B
CURRENT FILING DATE: 1997-04-21
PRIOR FILING DATE: 1997-04-21
PRIOR PLILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 302
SOFTWARE: Patentin version 3.1
SEQ ID NO 51
LENGTH: 447
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1.5e-114;
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100.0%; Pred. No. 1.5
tive 0; Mismatches
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; ORGANISM: hepatitis C virus
US-08-836-0758-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 447; Conservative
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US-09-374-494-51
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COMEDUTER: IBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Microsoft Word 6.0 / ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,138
FILING DATE: 0-0-MAY-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 9487016.9
FILING DATE: 4UNROWN-
FILING DATE: 28 Jun 1995
ATTORNEY/AGENT INFORMATION:
MANGE: KARMERER: PATRICIA A.
REGISTRATION NUMBER: 29,775
REGISTRATION NUMBER: 29,775
REGISTRATION NUMBER: 29,775
REGISTRATION SOR SEGION 0.51:
NEGISTRATION SOR SEGION 0.51:
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SEQUENCE DESCRIPTION: SEQ ID NO: 51:
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                                                          STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
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Best Local S:
Matches 447,
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Sequence 51, Application US/09851138
GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT

STUYVER, LIEVEN

TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES

AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
                                                                                                                                                                              US-09-374-494A-51

Sequence 51. Application US/09374494A

GENERAL INFORMATION:

TITLE OF INVENITON: Drophylactic, therapeutic and diagnostic agents.

TITLE OF INVENITON: Drophylactic, therapeutic and diagnostic agents.

TITLE OF INVENITON: New Sequences of hepatitis C virus genotypes and their use as TITLE OF INVENITON: NUMBER: US/09/374,494A

CURRENT PAPLICATION NUMBER: E 94870166.9

PRIOR FILING DATE: 1994-10-21

PRIOR FILING DATE: 1995-06-28

NUMBER OF SEQ ID NOS: 302

NUMBER OF SEQ ID NOS: 302

SOFTWARE PATENTIAL PARENTIAL PAR
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99.7%; Score 445.8; DB 21; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 447; Conservative 0; Mismatches 0; Indels 0;
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421 ACTGTCCAGGACTGCAACTGTTCCATC 447
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CORRESPONDENCE ADDRESS:
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US-09-374-494A-51
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US-09-851-138-51
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RESULT 8
US-08-836-075B-220
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GENERAL INFORMATION:
APPLICANT: INNOGENETICS N.V.
TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as TITLE OF INVENTION: prophylactic, therapeutic and diagnostic agents.
FILE REFERENCE: 2551-106
CURRENT APPLICATION NUMBER: US/09/851,138C
PRIOR PILING DATE: 1994-10-21
PRIOR FILING DATE: 1994-10-21
PRIOR APPLICATION NUMBER: EP 95870076.7
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Sequence 51, Application US/09851138B
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: New Sequences of hepatitis C virus genotypes and thei
TITLE OP INVENTION: New Sequences of hepatitis C virus genotypes and thei
TITLE OP INVENTION: Drophylactic, therapeutic and diagnostic agents.
FILE REFERENCE: 2551-106
CURRENT APPLICATION NUMBER: EP 94870166.9
FRICH APPLICATION NUMBER: EP 94870166.9
FRICH RIGHOR DATE: 1994-10-21
FRICH FILING DATE: 1994-10-21
FRICH FILING DATE: 1995-06-28
SOFTWARE: PARCH FILING DATE: 1995-06-28
SOFTWARE: PARCHIN VERSION 3.1
FRICH SEQ ID NOS: 302
SOFTWARE: PARCHIN VERSION 3.1
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1.5e-114;
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100.0%; Pred. No. 1...
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                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: hepatitis C virus
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.05
Matches 447; Conservative
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Sequence 220, Application US/08836075B
GENERAL INFORMATION:
APPLICANT: INNOGENETICS N.V.
TITLE OF INVENTION: Prophylactic, therapeutic and diagnostic agents.
TITLE OF INVENTION: prophylactic, therapeutic and diagnostic agents.
FILE REPRESENCE: 2551-105
CURRENT APPLICATION NUMBER: US/08/836,075B
CURRENT APPLICATION NUMBER: EP 94870166.9
PRIOR APPLICATION NUMBER: EP 94870166.9
PRIOR APPLICATION NUMBER: EP 95870076.7
PRIOR FILING DATE: 1994-10-21
PRIOR FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 302
SOGTWARE: Patentin version 3.1
SEQ ID NO 220
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99.7%; Score 445.8; DB 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 447; Conservative 0; Mismatches 0;
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Pred. No. 6e-61;
0; Mismatches 117;
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PRIOR FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 302
SOFTWARE: Patentin version 3.1
SEQ ID NO 51
LENGTH: 447
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Best Local Similarity 73.6%;
Matches 326; Conservative (
                                                                                                                       ) TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-851-138C-51
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Sequence 220, Application US/09851138B
GENERAL INFORMATION:
APPLICANT: INNOGENETICS N.V.
TITLE OF INVENTION: prophylactic, therapeutic and diagnostic agents.
CURRENT APPLICATION NUMBER: US/09/851,138B
CURRENT FILING DATE: 1994-10-21
FRIOR FILING DATE: 1994-10-21
FRIOR FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 302
SOFTWARE: Patentin version 3.1
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                                      ATCCCTGTGAGCCCYACCGTCGCCGTGAAGTCGCCCCTGCGCCCCCCACCGCCTCTCCCGC
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Pred. No. 6e-61;
0; Mismatches 117;
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Best Local Similarity 73.6%;
Matches 326; Conservative
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US-09-851-138B-220
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LENGTH: 957
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ITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as TITLE OF INVENTION: prophylactic, therapeutic and diagnostic agents.

ITLE OF INVENTION: prophylactic, therapeutic and diagnostic agents.

CURRENT APPLICATION NUMBER: US/09/374,494A

CURRENT APPLICATION NUMBER: US/09/374,494A

PRIOR APPLICATION NUMBER: EP 94870166.9

PRIOR FILING DATE: 1994-10-21

PRIOR PILING DATE: 1994-10-21

PRIOR PLING DATE: 1995-06-28

NUMBER OF SEQ ID NOS: 30.2

SOFTWARE: Patentin Version 3.1

SEQ ID NOS: 30.2
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Pred. No. 6e-61;
0; Mismatches 117;
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Best Local Similarity 73.6%;
Matches 326; Conservative
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TYPE: DNA
CRGANISM: hepatitis C virus
US-09-374-494A-218
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Matches 323; Conservative
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US-09-374-494A-218
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LENGTH: 957
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ITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as TITLE OF INVENTION: New Sequences of hepatitis C virus genotypes and their use as TITLE OF INVENTION: prophylactic, therapeutic and diagnostic agents.

FILE OF INVENTION: prophylactic, therapeutic and diagnostic agents.

CURRENT PAPLICATION NUMBER: US/09/851,138C

CURRENT FILING DATE: 1094-10-20

PRIOR PILING DATE: 1994-10-21

PRIOR PILING DATE: 1994-10-28

NUMBER OF SEQ ID NOS: 302

SOFTWARE: PATENTI NOS: 302

SOFTWARE: PATENTI NOS: 302

SED ID NO 220

LENGTH: 957
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GENERAL INFORMATION:
APPLICANT: INNOGENETICS N.V.
TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as TITLE OF INVENTION: prophylactic, therapeutic and diagnostic agents.
FILE REFERENCE: 2551-105
CURRENT APPLICATION NUMBER: US/08/836,075B
CURRENT FILING DATE: 1997-04-21
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898 ACCGTCCAGTTGTGCAATTGCTC 920
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                                                                                                                   Sequence 220, Application US/09851138C GENERAL INFORMATION:
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US-08-836-075B-218
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ATTLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as TITLE OF INVENTION: prophylactic, therapeutic and diagnostic agents. FILE REFERENCE: 46 USdiv1
CURRENT APPLICATION NUMBER: US/09/374,494A
PRIOR APPLICATION NUMBER: EP 94870166.9
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 302
SOFTWARE: Patentin version 3.1
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Pred. No. 6.2e-60;
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1; Mismatches 119;
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PRIOR APPLICATION NUMBER: EP 94870166.9
PRIOR FILING DATE: 1994-10-21
PRIOR APPLICATION NUMBER: EP 95870076.7
PRIOR FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 302
SOFTWARE: Patentin version 3.1
SEQ ID NO 218
LENGTH: 957
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GENERAL INFORMATION:
APPLICANT: INNOGENETICS N.V.
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CURRENT APPLICATION NUMBER: US/09/851,138C
CURRENT FILING DATE: 2001-05-09
PRIOR FILING DATE: 1994-10-21
PRIOR FILING DATE: 1994-10-21
PRIOR FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 302
SOFTWARE: PatentIn version 3.1
SEQ ID NO 218
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APPLICANT: INNOGENETICS N.V.
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US-09-851-138C-218
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Matches 323; Conservative
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APPLICANT: INNOGENETICS N.V.
APPLICANT: INNOGENETICS N.V.
APPLICANT: INNOGENETICS N.V.
TITLE OF INVENTION: DEOPHYLACTIC, therapeutic and diagnostic agents.
TITLE OF INVENTION: DEOPHYLACTIC, therapeutic and diagnostic agents.
FILE REFERENCE: 2551-106
CURRENT APPLICATION NUMBER: US/09/851,138B
CURRENT FILING DATE: 1994-10-21
PRIOR APPLICATION NUMBER: EP 94870166.9
PRIOR PILING DATE: 1994-10-21
PRIOR FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 302
SOFTWARE: Patentin version 3.1
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The sequences AAT27937-T27989 represent novel sequences isolated from hepatitis C virus subtypes different from subtypes la-c, 2a-d, 3a-f, 4a-f, 5a and 6a. They esp. from the novel subtypes ld-f, 2e-1, 2k, 2l, 3g, 4k-m, 7a-c or types 9, 10 or 11. The sequences corresp. to the 5' untranslated region (UR), the Core/El, NG4 or NSSB regions of the genome. This sequence represents nucleotides 478-925 from the HCV type 10a
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Aaz07652 H
Aaq78081 H
Aaq78106 H
                                                                                                       March 4, 2005, 09:20:58; Search time 1057 Seconds
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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isolate NE98. The new HCV types were isolated from patients with chronic they from the Benelux countries, France, Cameroon and Vietnam, because of their aberrant reactivities. The RNA was extracted, cDNA synthesised and PCR amplified, cloned and genotyped. The S'UR, Core/E1 and NSBB regions were sequenced either directly or partially and used to classify the new Yuruses into (sub) types based on comparison with known sequences. The sequences were used to generate the peptides AAR96424-R96524. The sequences can also be used to synthesise probes and primers for the detection of HCV in a sample. The polypeptides can be used to detect anti-HCV antibodies, for HCV typing or to prevent HCV infections
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                                                                                                                                                                                                                                           Length 447;
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                                                                                                                                                                                                  Sequence 447 BP; 82 A; 130 C; 114 G; 118 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                             Indels
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    /*tag= a
    /product= "Core/El polypeptide."

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Compositions comprising at least 5, and pref. 8 or more contiguous nucleotides selected from an HCV type 3 genomic sequence, more particularly (1) the region spanning positions 417-957 of the Core/El region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of the NS3 region of HCV type 3; (iii) the region spanning positions 4892-529 of the NS3/4 region of HCV type 3; (iv) the region spanning positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to an isolate belonging to a specific genotype, or as a probe for specific detection/lassification of nucleic acid. Polypeptides encoded by the nucleotides in such compositions may be used for smoothand for sequence consesponds to the Core/El region of HCV and for serotyping. This sequence corresponds to the Core/El region of HCV aubtype 3a and is taken from a clone designated HDI0-2-21.
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Pred. No. 1.3e-63;
1; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 107-108; 404pp; English
                                                        93EP-00401099.
     94WO-EP001323
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Matches 313; Conserv
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27-APR-1994;
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AGGCATGTAGACATATTGGTGGCGCGCGACGATGTGCTCTGCTCTACGTGGGGGGAT 420

CTTTGTGGAGCGCTATTTCTTGTYGGGCAGGGTTCTCATGGAGACATCGCCAGCATTGG

ACTGTCCAGGACTGCAACTGTTC 443

420

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ACCCACCTGGATATGATGGTGGGRGCGGCCACCTATGCTCAGCTCTACCTAGGAGAC 360
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                                         CTCTACATGGTAACTAACGACTGCAGTAACGGTAGTATCGTGTATGAGGCCGGGGATATT
                                                                                                                    Compositions comprising at least 5, and pref. 8 or more contiguous nucleotides selected from an HCV type 3 genomic sequence, more particularly (1) the region spanning positions 417-957 of the Core/El
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classification, immunisation, prophylaxis, serotyping, ss.
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01-AUG-1995
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Polypeptides encoded by the nucleotides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV subtype 3a and is taken from a clone designated HD10-2-5.

(Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; primer; probe; detection; diagnosis; classification; immunisation; prophylaxis; serotyping; ss.
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1larity 70.7%; Pred. No. 1.3e-63;
Conservative 1; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
2. .541
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/product= "Core/El polypeptide."
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                                                                          AAQ78029 standard; cDNA; 541 BP
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93EP-00402019
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(first entry)
                                                                                                                                                                                                                                                                                                                 Hepatitis C virus type 3a.
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05-AUG-1993;
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20-JUL-1995
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Query Match

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region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of the NS3 region of HCV type 3; (iii) the region spanning positions 4892-522 of the NS3/4 region of HCV type 3; (iv) the region spanning positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype amplify nucleic acid from an isolate belonging to a specific genotype, or as a probe for specific detection/classification of nucleic acid.

Polypeptides encoded by the nucleocides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV and for serotyping. This sequence corresponds to the Core/E1 region of HCV subtype 3a and is taken from a clone designated BR36-9-20. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                         Indela
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Pred. No. 4.1e-63;
1; Mismatches 130;
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Compositions comprising at least 5, and pref. 8 or more contiguous nucleotides selected from an HCV type 3 genomic sequence, more particularly (1) the region spanning positions 417-957 of the New Core/El region of HCV subtype 3; (ii) the region spanning positions 464-4730 of the NS3 region of HCV type 3; (iii) the region spanning positions 4892-5292 of the NS34 region of HCV type 3; (iv) the region spanning positions 8023-825 of the NS5 region of the BR36 subgroup of HCV subtype 3; or (v) an HCV subtype 3c genomic sequence, may be used as primers to amplify nucleic acid from an isolate belonging to a specific genotype, or as a probe for specific detection/classification of nucleic acid. Polypeptides encoded by the nucleotides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV subtype 3a and is taken from a clone designated BR33-1-20. (Updated on 25-MAR-2003 to correct PN field.)
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05-AUG-1993;
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P-PSDB; AAR63278.
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05-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compositions comprising at least 5, and pref. 8 or more contiguous nucleotides selected from an HCV type 3 genomic sequence, more particularly (1) the region spanning positions 417-957 of the Core/E1 region of HCV subtype 3; (11) the region spanning positions 4664-4730 of the NS3 region of HCV type 3; (11) the region spanning positions 4892-5129. Of the NS3/4 region of HCV type 3; (14) the region spanning positions 4892-513. Of the NS3/4 region of HCV subtype 3; (14) the region spanning positions 4892-513. Of the NS3 region of the BR36 subgroup of HCV subtype 3; (14) the region spanning positions 4892-513. Or (14) an HCV subtype 3 genomic sequence, may be used as primers to amplify nucleic acid from an isolate belonging to a specific genotype, or as a probe for specific detection/classification of nucleic acid. Polypeptides encoded by the nucleocides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV and for serotyping. This sequence corresponds to the Core/E1 region of HCV subtype 3a and is taken from a clone designated BR36-9-13. (Updated on 25-MAR-2003 to correct PN field.)
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Hepatitis C virus Core/El region.
                                                                                                                          AAQ78032 standard; cDNA; 541 BP
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Best Local Similarity 70.4<sup>3</sup>
Matches 312, Conservative
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P-PSDB; AAR63280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-APR-1993;
05-AUG-1993;
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                                                                                                                                                                                                         25-MAR-2003
01-AUG-1995
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ઠે 셤 /product= "Core/El polypeptide."

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nucleotides selected from an HCV type 3 genomic sequence, more particularly (i) the region spanning positions 417-957 of the Core/E1 region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of the NS3 region of HCV type 3; (iii) the region spanning positions 4892-529 of the NS3 region of HCV type 3; (iv) the region spanning positions 4892-320 of the NS3 region of the BR36 subgroup of HCV subtype 3c of the NS5 region of the BR36 subgroup of HCV subtype 3c of the NS5 region of the BR36 subgroup of HCV subtype 3c of the NS5 region of the BR36 subgroup of HCV subtype 3c of an isolate belonging to a specific genotype, or amplify nucleic acid from an isolate belonging to a specific genotype, or as a probe for specific detection/classification of nucleic acid. For immunisation against HCV, for the detection of antibodies directed against HCV and for serotyping. This sequence corresponds to the Core/E1 region of HCV subtype 3a and is taken from a clone designated HDIO-2-14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTTGTTCTCATGCTTGCTTACACCCACAGCCGGGCTGGAGTACCGTAATGCCTCCGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 233; DB 2; Length 54
Pred. No. 1.3e-62;
1; Mismatches 131; Indels
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Compositions comprising at least 5, and pref. 8 or more contiguous nucleotides selected from an HCV type 3 genomic sequence, more particularly (i) the region spanning positions 417-957 of the No. Control of HCV type 3; (ii) the region spanning positions 464-4730 of the NS3 region of HCV type 3; (iii) the region spanning positions 4892-520 of the NS34 region of HCV type 3; (iv) the region spanning positions 4892-620 of the NS34 region of HCV type 3; (iv) the region spanning positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype 3; or (v) an HCV subtype 3c genomic sequence, may be used as primers to as in some sequence, may be used as primers to as a probe for specific detection/classification of nucleic acid. Polypeptides encoded by the nucleocides in such compositions may be used for specific against HCV, for the detection of antibodies directed against HCV and for serotyping. This sequence corresponds to the Core/E1 region of HCV subtype 3a and is taken from a clone designated BR33-1-i0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide sequences from hepatitis C virus - and related vectors, polypeptide(s) and antibodies, useful for immunisation, treatment, diagnosis and typing of HCV isolates.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.1%; Score 233; DB 2; Length 54 70.2%; Pred. No. 1.3e-62; ive 1; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 113-114; 404pp; English
                                                                                                                                              93EP-00401099.
                                                                                                              94WO-EP001323
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Conservative
                                                                                                                                                                                                    (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                        Maertens G, Stuyver L;
                                                                                                                                                                                                                                                                        WPI; 1994-358277/44
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es 311; Conserv
                                                                                                                                                                                                                                                                                           P-PSDB; AAR63282
                                        WO9425601-A2
                                                                                                            27-APR-1994;
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Location/Qualifiers

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Hepatitis C virus type 3a.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compositions comprising at least 5, and pref. 8 or more contiguous nucleotides selected from an HCV type 3 genomic sequence, more particularly (1) the region spanning tositions 417-957 of the Nore Fedion spanning positions 4664-4730 of the NS3 region of HCV type 3; (ii) the region spanning positions 4892-559. Of the NS3/4 region of HCV type 3; (iv) the region spanning positions 4892-519. Of the NS3/4 region of HCV type 3; (iv) the region spanning positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype 3s or (v) an HCV subtype 3c genomic sequence, may be used as primers to amplify nucleic acid from an isolate belonging to a specific genotype, or position of specific detection/classification of nucleic acid. Polypoptides encoded by the nucleocides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed significant HCV and for secotyping. This sequence corresponds to the Core/E1 region of HCV subtype 3a and is taken from a clone designated BR33-1-19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide sequences from hepatitis C virus - and related vectors, polypeptide(s) and antibodies, useful for immunisation, treatment, diagnosis and typing of HCV isolates.
                                                                                                                                                                                                                                                Hepatitis C virus; HCV; primer; probe; detection; diagnosis; classification; immunisation; prophylaxis; serotyping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.1%; Score 233; DB 2; Length 54 Best Local Similarity 70.2%; Pred. No. 1.3e-62; Matches 311; Conservative 1; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                      /product= "Core/El polypeptide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 115-116; 404pp; English.
              443
                            Location/Qualifiers
2..541
/*tag= a
                                                                                                                                                                                                                   Hepatitis C virus Core/El region.
          ACTGTCCAGGACTGCAACTGTTC
                                                                                                                AAQ78035 standard; cDNA; 541 BP
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93EP-00402019
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                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                              Hepatitis C virus type 3a.
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                                                                                                                                                                            (revised)
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01-AUG-1995
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                                                                                                                                                                                                                                                                              361
                                                                                                                                                                                                                                                                                                                                                          362 AGTCATGTGGACCTGTTAGTAGGCGCGCCACGATGTGCTCTGCGCTTTACGTGGGTGAT 421
                                                                                                                                                                                                                                                                                                                                                                                                      CTTTGTGGAGCGCTATTTCTTGTYGGCCAGGGTTCTCATGGAGACATCGCCAGCATTGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                              422 ATGTGTGGGGCCGTCTTCCTCGTGGGACAAGCCTTCACGTTCAGACCCCGCCGCCGTCAA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT12704-T12709 and AAT12961-T12974 represent hepatitis C virus (HCV) E1 and E2 protein coding sequence constructs. These sequences are included in vectors for the production of recombinant E1, E2, and E1/E2 proteins. The recombinant proteins can then be isolated using a method of the invention. In the method, the envelope proteins are purified by carrying out a disulphide bond cleavage, or a reduction step with a disulphide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human; serotype; reversed phase hybridisation assay; genotype; antigen; sera;
                       302 ACCCCAGTAAACACCTACAGTAGAGGAGAACGTCGGGGCAACCACCGCTTCGATACGC
                                                                             CTCTACATGGTAACTAACGACTGCAGTAACGGTAGTATCGTGTATGAGGCCGGGGATATT
                                                                                                                   182 CTCTATGTCCTTACCAACGACTGTTCCAATAGTAGTATTGTGTATGAGGCCGATGACGTT
                                                                                                                                                           ATCCTCCACTTACCTGGCTGTGTCCCCTGCGTACGCTCTGGCAATACATCAAGATGCTGG
                                                                                                                                                                                                 <u>Arrerscaegecececeserstrandranererecaegaegecarracerecraege</u>
                                                                                                                                                                                                                                         ACGCACGTGGATATGATGGTGGGGGCCACCCTATGCTCAGCTCTCTACGTAGGAGAC
GCTTTGTTCTCATGCTTGCTTACACCCACAGGCCGGGCTGGAGTACCGTAATGCCTCCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 CTTTGTGGAGGGGTATTTCTTGTYGGGCAGGGGTTCTCATGGAGACATGGCCAGCATTGG 420
                 constructs containing the purified HCV envelope proteins can be used for vaccinating humans against HCV, for in vitro detection of HCV antibodies in a sample, and in a servityping assay for detecting one or more serological types of HCV present in a biological sample. The constructs can also be immobilised on a solid substrate and incorporated into a reversed phase hybridisation assay for determining the presence or the genotype of HCV. The new purification method preserves the conformation of the recombinantly expressed E1, E2 and E1/E2, and eliminates contaminating proteins. Antigens isolated using this method are more reactive with human sera than those isolated by known techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTCTGTTCTTCTTCATCATCAGCAGCTAGTCTAGAGTGGCGGAATACGTCTGGC 243
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  cleavage agent, after lysis of recombinant host cells. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus, HCV, El protein; E2 protein; infection; gene, virucide; immunostimulant; vaccine; ds.
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0
                                                                                                                                                                                                                                                                                                                                       Length 630;
                                                                                                                                                                                                                                                                                    Sequence 630 BP; 127 A; 175 C; 168 G; 160 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                  52.1%; Score 233; DB 2; 70.2%; Pred. No. 1.4e-62;
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The present invention relates to new therapeutic vaccine compositions for inducting hepatitis C virus (HCV)-specific antibodies, comprising a composition containing at least one purified recombinant HCV single or specific oligomeric recombinant envelope proteins selected from an B1 and an B2 protein, and optionally a pharmaceutical adjuvant. The vaccines are useful for inducing HCV-specific antibodies or for immunising humans against HCV. The recombinant HCV screening and confirmatory antibody tests, for raising antibodies, in HCV screening and confirmatory antibody tests, for raising antibodies, in the preparation of medicament, and for in vitro monitoring of HCV disease or prognosing the response to treatment of patients suffering from HCV infection. The present sequence is a coding sequence described in the exemplification of the invention
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                                                                                                                                                                                                                                                                                Hepatitis C virus, HCV, vaccine, liver disease, El protein, E2 protein, liver fibrosis, ds, gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 233; DB 10; Length 6
Pred. No. 1.4e-62;
1; Mismatches 131; Indels
                                                                                                                                                             Hepatitis C virus E1/E2 protein coding sequence #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence encodes an HCV E1/E2 protein
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16-OCT-2002; 2002US-0418358P.
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Best Local Similarity 70.2%;
Matches 311; Conservative :
                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus.
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                                                15-JAN-2004
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The invention relates to the use of a hepatitis C virus (HCV) vaccine composition for reducing liver disease (such as liver fibrosis or its progression), serum alanine maintoransferase (ALT) levels, steatosis, or anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal, conformally a chronic HCV-infected mammal. The liver disease is reduced by at least 1-2 points according to the overall lshk score in the HCV-infected mammal. Also included are a method for predicting charges in liver disease in a chronic HCV-infected mammal, a therapeutic charges in liver disease in a chronic HCV-infected mammal, a therapeutic charges in liver disease from an all or E2 protein composition (comprising at least one purified or a combination of at least 2 HCV single or specific oligomeric recombinant E1 complex formed from purified HCV single or specific oligomeric recombinant E1 or E2 protein or complex formed from purified HCV single or specific oligomeric recombinant E1 or E2 proteins or its parts and optionally, a pharmaceutical adjuvant), and immunogenic HCV composition (or HCV vaccine composition) comprising a recombinant virus allowing expression of at least one HCV recombinant crossition of at least one HCV recombinant envelope protein despete from man E1 protein and/or an E2 protein composition of the E1 and E2 protein and/or an E2 protein composition is cof at least one HCV recombinant envelope protein choosition is cof at least one HCV recombinant envelope protein choosition is cof at least one HCV recombinant envelope protein choosition is coptionally, a pharmaceutical adjuvant. The HCV vaccine composition is protein and/or an E2 protein, and parts of the E1 and E2 proteins and or the liver in a chronic HCV-infected mammal, particularly human. The HCV vaccine composition is cuseful for reducing liver disease (such as liver fibrosis or its profered mammal, particularly human. The HCV broaching account in vitco monitoring HCV disease or prognosing the response to treatment of patients suffecting from HCV in
                                                                                                                                                                                Hepatitis C virus, HCV; El glycoprotein; E2 glycoprotein; HCV infection, liver disease; liver fibrosis; 88; serum alanine aminotransferase level; steatosis; anti-E2 immunoreactivity; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of hepatitis C virus (HCV) vaccine composition for reducing liver disease, serum alanine aminotransferase levels, steatosis, or anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 29; 176pp; English.
                                                                                                                                      HCV DNA encoding El protein HCC162.
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ADP71119 standard; cDNA; 630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-2001; 2001US-0453708P.
16-OCT-2002; 2002US-0418358P.
                                                                                                                                                                                                                                                                     Hepatitis C virus; type 3a.
                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MAER/) MAERTENS G
(DEPL/) DEPLA E.
(BOSM/) BOSMAN F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; ADP71120
                                                                                                                                                                                                                                                                                                                    US2004126395-A1
                                                                                         23-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maertens G,
                                                                                                                                                                                                                                                                                                                                                               01-JUL-2004.
                                            ADP71119;
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of hepatitis

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The invention provides two new isolates of hepatitis C virus (HCV), J1 and J7. These two isolates comprise nucleotide and amino acid sequences that are distinct from the HCV isolate HCV.1. The nucleotide sequences may be used to detect non-A, non-B HCV (NANBH) polynucleotides by hybridisation for diagnosis of NANBH infections. They may also be used to soreen blood and blood products for this infection. The isolates may also be used to isolate other naturally occurring variants of the virus. The polypeptides may be used as a vaccine for wariants of the virus. The polypeptides may be used as a vaccine for present sequence represents the NSI domain consensus sequence of HCV isolates J1 and HCV-1. (Updated on 20-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                             68 GACGGCGTGAACTATGCAACAGGAAXYTKCCYGGTTGCTCTTTCTCTATCTTCCCTYYTG 127
                                                                                                                                                                                                                                                                                                                                                                                 241 ATCCCTGTGAGCCCYACCGTCGCCGTGAAGTCGCCCTGCGCCGCCACCGCCTCTCTCCGC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCTACATGGTAACTAACGACTGCAGTAACGGTAGTATCGTGTATGAGGCCGGGGATATT
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                                                                                                                                                                                                                                                                               Length 1249;
                                                                                                                                                                                                                                                   Sequence 1249 BP; 160 A; 282 C; 276 G; 206 T; 0 U; 325 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Envelope; region; type C; hepatitis; virus; HCV; vaccine;
non-A, non-B; amplify; ss.
                                                                                                                                                                                                                                                                                                        Indels
                      for diagnosis
                                                                                                                                                                                                                                                                                           ; Pred. No. 8.2e-59;
83; Mismatches 120;
                                                                                                                                                                                                                                                                               49.5%; Score 221.4; DB 2;
                     Hepatitis C Virus isolates, useful
                                infections and development of vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTGTCCAGGACTGCAACTGTTCCATC
                                                        Disclosure, Fig 14; 132pp; English.
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Matches 244; Conservative
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                                         Length 630;
              G; 160 T; 0 U; 0 Other;
                                                                 Indels
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                                      Score 233; DB 12;
Pred. No. 1.4e-62;
1; Mismatches 131;
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              Sequence 630 BP; 127 A; 175 C; 168
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89US-00456142.
90EP-00310149.
                                      52.1%;
70.2%;
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(first entry)
                                                   Best Local Similarity ,v...
Matches 311; Conservative
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HCV infection; vaccine;
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Cha T, Irvine BD;
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CHIRON CORP.
                                                 Local Similarity
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21-DEC-1989;
17-SEP-1990;
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487

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GCTTTGTTCTCATGCTTGCTTACACCCACAGCCGGGCTGGAGTACCGTAATGCCTCCGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 565;
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Best Local Similarity 45.2%; Pred. No. 2.5e-58;
Matches 202; Conservative 143; Mismatches 102; Indels
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                                                                                                                                                                                                                                   Claim 1; Page 2; 13pp; Japanese
                                                              91JP-00152169
                                                                                           91JP-00152169
                                                                                                                                                       WPI; 1993-022708/03
                                                                                                                        (TEIJ ) TEIJIN LTD.
                                                              29-MAY-1991;
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                               04-DEC-1992
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. March 4, 2005, 11:12:53 ; Search time 2352 Seconds (without alignments) 7234.153 Million cell updates/sec igence: 447 serfect score: 447 sequence: 1 gacggaattaattcgcaacaggactgcaactgttccatc 447 scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0 searched: 34239544 segs, 19032134700 residues Octal number of hits satisfying chosen parameters: 68479088	Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% 1, isting first 45 summaries	t1:* t2:* t2:* t3:* t4:* t5:* t5:* t6:* s2:* s2:* mber of results or equal to the nalysis of the t	# Query Growth DB ID Description Descripti

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/mol_type="mRNA"
/mol_type="mRNA"
/mol_txpe="ATCC 30984"
/db_xref="taxon:108607"
/clone lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 TCCTCCACTTACCTGGCTGTGTCCCCTGCGTACGCTCTGGCAATACATCAAGATGCTGGA 241
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rockefeller.0.341 Mastigamoeba balamuthi lambda ZAP II Library
Mastigamoeba balamuthi cDNA similar to elongation factor 1 alpha,
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                                                                                                                                                                                                                                                                                                                                                                                                       The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
                                                                                                                                                                                                                                                   Eukaryota, Pelobiontida, Mastigamoebidae, Mastigamoeba.
1 (bases 1 to 1559)
Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and Philippe, H.
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Mastigamoeba balamuthi
Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 1561)
Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W.,
Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
Philippe, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Aug 25, 2000 this sequence version replaced gi:9919779. Contact: Muller Miklos Laboratory of Biochemical Parasitology The Rockefeller University
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llarity 50.8%; Pred. No. 0.33;
Conservative 1; Mismatches 95; Indels 0
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Email: mmuller@rockvax.rockefeller.edu
Insert Length: 1559 Std Error: 0.00
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Mastigamoeba balamuthi
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Mastigamoeba balamuthi cDNA similar to elongation factor 1 alpha,
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/strain="ATCC 30984"
/db_xref="Haxon:108607"
/clone_lib="mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
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The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostellum, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
                       TCTTGTYGGGCAGGGGTTCTCATGGAGACATCGCCAGCATTGGACTGTCCAGGACTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mastigamoeba balamuthi
Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 1517)
Bapteste,E., Brinkman,H., Lee,J.A., Moore,D.V., Sensen,C.W.,
Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
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Contact: Muller Miklos
Laboratory of Biochemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 1517 Std Error: 0.00
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/clone_lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="gyn: Phreatamoeba balamuthi"
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Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 270)
Bapteste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W.,
Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
Philippe,H.
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//organism="Mastigamoeba balamuthi"
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/etrain="ATCC 30984"
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Best Local Similarity 49.2%; Pred. No. 2.1;
Matches 96; Conservative 0; Mismatches 99;
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The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Bamil: mmuller@rockvax.rockefeller.edu
Insert Length: 270 Std Error: 0.00
POLYA=Yes.
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/clone_lib="Mastigamoeba
/note="syn: Phreatamoeba
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Mastigamoeba balamuthi
Babtaryota, Pelobiontida; Mastigamoebidae; Mastigamoeba.

1 (bases 1 to 562)
Bapteste, B., Brinkmann, H., Lee, J. A., Moore, D. V., Sensen, C. W.,
Bapteste, B., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
Philippe, H.

The analysis of 100 genes supports the grouping of three highly
divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba
Proc. Natl. Acad. Sci. U.S. A. 99 (3), 1414-1419 (2002)
The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002) 21819461
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The Rocksfeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rocksfeller.edu
Insert Length: 552 Std Error: 0.00
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TCGGTGTCATCAAGACCGTCGTCGCCAAGGTCCCCGGCAAGACCGGTGCCGCCGGGGGAA 87
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Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
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Pred. No. 3.9;
1; Mismatches 60; Indels (
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Laboratory of Blachemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, t
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 409 Std Error: 0.00
POLYA=Yes.
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Best Local Similarity 54.8%;
Matches 74; Conservative
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                                                                                                                                                                                                             The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
Mastigamoeba balamuthi
Mastigamoeba balamuthi
Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.

1 (bases 1 to 482)
Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and Philippe, H.
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Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 571)
Bapteste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W.,
Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
Philippe,H.
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8.6%; Score 38.6; DB 4; Length 482;
Best Local Similarity 54.8%; Pred. No. 4;
Matches 74; Conservative 1; Mismatches 60; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     usa
                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory of Biochemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, t
Bmail: mmuller@rockvax.rockefeller.edu
Insert Length: 482 Std Error: 0.00
POLYA=Yes.
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Laboratory of Biochemical Parasitology
The Rockefeller University
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Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae; Oryzae;

Ehrhartoideae; Oryzae;

I (bases 1 to 1416)

Mang. J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G.K.S., Deng, X.W. and Wang, J.

An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

Unpublished (2004)

Contact: Chen Chen

Department of Bioinformatic

Beijing Institute of Genomice

Chinese Academy of Sciences, Beijing 101300, China

Tel: 86-10-80488670

Email: chenche@genomics.org.cn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1416 bp DNA linear GSS 21-SEP-2004 OSIFCCO06646 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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                                                                                                                                                                         470 AGAAGGACGCCAAGAAGAAGAGAGCGCCGCTCCTTGCTCTGCAACCTCTCTAAGAGAGC 529
                                 CGCACGTGGATATGATGGTGGGRGCGGCCACCCTATGCTCAGCTCTCTACGTAGGAGACC 361
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53.0%; Pred. No. 4.9;
ative 1; Mismatches 70;
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BM321414
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/organism="Mastigamoeba balamuthi"
/mol typa="mRNA"
/strain="ATCC 3084"
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Mastigamoeba balamuthi
Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 650)
Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W.,
Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
Philippe, H.
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54.8%; Pred. No. 4.2;
ive 1; Mismatches 60; Indels
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    650
    organism="Mastigamoeba balamuthi"

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8.6%; Score 38.6; DB 2;
Best Local Similarity 54.8%; Pred. No. 4.1;
Matches 74; Conservative 1; Mismatches 60;
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Laboratory of Biochemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, U
Emall: mmuller@rockvax.rockefeller.edu
Insert Length: 650 Std Error: 0.00
                              Email: mmuller@rockvax.rockefeller.edu
Insert Length: 571 Std Error: 0.00
POLYA=Yes.
.230 York Avenue, New York, NY 10021,
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found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                  http://image.llnl.gov
Plate: LLCM2384 row: i column: 12
High quality sequence stop: 644.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.4%; Score 37.4; 64.4%; Pred. No. 10;
                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 CACAGCCGGGCTGGAGTACCGTAATGC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 GTCACCCAGGCTGGAGTGCAGTGCTGC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/db_xref="GDB:425661"
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Matches 56; Conserv
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H29400
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AGENCOURT_1983174 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215507
BQ707541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mastigamoeba balamuthi"
/mol_type="mRNA"
/strain="ATCC 30984"
/db_xref="taxon:108607"
/clone_llb="Mastigamoeba balamuthi lambda ZAP II Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 924)

                                                                                                                                                                                                         The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
                                                                         Mastigamoeba balamuthi
Mastigamoeba balamuthi
Eukaryota, Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 1538)
Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W.,
Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 CGCACGTGGATATGATGGTGGGRGCGGCCACCCTATGCTCAGCTCTTACGTAGGAGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.6%; Score 38.6; DB 2; Length 1538;
4.8%; Pred. No. 4.9;
ve 1; Mismatches 60; Indels 0
                                                                                                                                                                                                                                                                                                                                       Laboratory of Biochemical Parasitology
The Rockefeller University
Jajo York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 1538 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      Contact: Muller Miklos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ707541.1 GI:21846440
                                   BE636716.1 GI:9919827
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Matches 74; Conservative
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sequence.
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/mol_type="mRNA"
/mol_type="mRNA"
/db_tref="twaxon:9606"
/clone="twaxon:9606"
/lab_host="DH10B (phage-resistant)"
/clone=lib="will MGC 113"
/clone=lib="will MGC 113"
/note="forgan: spleen; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/AhoI sites using the following 5; adaptor:
GGACGAGIG. Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@wateon.wustl.edu
Insert 51ze: 1974
High quality sequence stops: 319 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1974 Std Error: 0.00
Seq primer: M13RPI
High quality sequence stop: 319.
Location/Qualifiers
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ym60b07.r1 Soares infant brain INIB Homo sapiens cDNA clone
IMAGE:52725 5', mRNA sequence.
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(Dassa 1 to 458)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Leo,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Wed

/db_xref="taxon:9606" /clone="IMAGE:52725"

'sex="female"

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/db_xref="taxon:0031"
/clone="pgp2n.pk002.n18"
/sex="male and Female"
/fissue type="pituitary Gland/Hypothalamus/Pineal Gland"
/dev stage="Embryonic (d12,d14,d19); post-hatch (1,3,5,7,9 week8)"
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1 (bases 1 to 555)
Porter, T.E. and Cogburn, L.A.
ESTS from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA library, USDA/IFAPS Animal Genome Project
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/strain="Commercial broiler chickens"
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/clone_lib="Normalized Chicken
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University of Delaware
Townsend Hall, Newark, DE 19717, USA
TE1: 302-831-1332
Fax: 302-831-2822
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BM490244.1 GI:18611175
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Gallus gallus
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